

ATCTCTCTCTCACAGAGATTGTAACCTTCACGCACACGTAACCTAAATCGAAGATGGTG 60  
M V 2

AGAAAATATAGAAAAGCTAAAGGAATTGTAGAAGCTGGAGTTTCGTCAACGTATATGCAG 120  
R K Y R K A K G I V E A G V S S T Y M Q 22

CTACGGAGCCCGGAGAATTGTTTATGTTAGATCGGAAAAATCAAGCTCTGTCTCCGTCGTC 180  
L R S R R I V Y V R S E K S S S V S V V 42

GGTGATAATGGAGTTTCGTCTGTTGTAGTGGAAGCAATGAATATAAGAAGAAAGAATTA 240  
G D N G V S S S C S G S N E Y K K K E L 62

VI VII

ATACATCTGGAGGAGGAAGATAAAGATGGTGACACTGAAACGTCGACGTATCGACGGGGT 300  
I H L E E E D K D G D T E T S T Y R R G 82

ACGAAGAGGAAGCTTTTTGAAAATCTGAGAGAGGAGGAGAAAAGAAGAAATTAAGTAAATCC 360  
T K R K L F E N L R E E E K E E L S K S 102

ATGGAGAATTATTCATCGGAATTTGAATCGCGGGTTAAAGAATCGTTAGATTGTTGTTGT 420  
M E N Y S S E F E S A V K E S L D C C C 122

AGCGGGAGGAAAACGATGGAGGAGACGGTGACGGCGGAGGAGGAGAAGCGGAAATTG 480  
S G R K T M E E T V T A E E E E K A K L 142

ATGACGGAGATGCCAACGGAATCGGAAATTAAGATTTTTTTGTGGAAGCTGAGAAACAA 540  
M T E M P T E S E I E D F F V E A E K Q 162

VIII

CTCAAAGAAAAATTCAAGAAGAAGTACAATTTTCGATTTTCGAGAAGGAGAAGCCATTAGAA 600  
L K E K F K K K Y N F D F E K E K P L E 182

GGACGTTACGAATGGGTAAAGTTAGAGTGAAGAAGAAGAAGTTTATGGTTTTTTTTT 660  
G R Y E W V K L E . 191

TAACTTTTTAGATTTTAATATTTTCAGGGAATAAGTTAATTTTATTTTGTGATTGGA 720

TATAAGATTGTAGGAGGAATGTTTTTAGAAGTACGAAATGCACAGAAAAGAAGAAAG 780

CTTTTAAACAGATTTTAGAGCCCAGAAAAGTCGTGTCTTTTAGCTCTACTTTTACCTCTT 840

CTTCGAATCTTGTGTATCTTTTAGCATATCTTTAGTACATTTTATGTTTTTGGTGA 900

GATA\* 905

Characterization of cDNA (Wang et al., 1997) and genomic sequences of *ICK1*.  
**(A).** Genomic organization *ICK1*. Open bars represent exons and filled bars, introns.  
**(B).** Features of cDNA sequence and deduced amino acid sequence.

Figure 1

61 ACGTATATGCAGCTACGGAGCCGGAGAATTGTTTATGTTAGATCGGAAAAATCAAGCTCT Ick1.seq  
 3 ACGTATATGCAGCTACGGAGCCGGAGAATTGTTTATGTTAGATCGGAAAAATCAAGCTCT ICK1b.seq  
 6 GATTGTTT TAG ICK1c.seq

121 GTCTCCGTCGTCGGTGATAATGGAGTTTCGTCGCTTGTAGTGGAGCAATGAATATAAG Ick1.seq  
 63 GTCTCCGTCGTCGGTGATAATGGAG ICK1b.seq  
 18 ICK1c.seq

181 AAGAAAGAATTAATACATCTGGAGGAGGAAGATAAAGATGGTGACACTGAAACGTCGACG Ick1.seq  
 88 ICK1b.seq  
 18 ICK1c.seq

241 TATCGACGGGTACGAAGAGGAAGCTTTTGAATCTGAGAGAGGAGGAGAAAGAAGAA Ick1.seq  
 88 ICK1b.seq  
 18 GGGTACGAAGAGGAAGCTTTTGAATCTGAGAGAGGAGGAGAAAGAAGAA ICK1c.seq

301 TTAAGTAAATCCATGGAGAATTATTCATCGGAATTTGAATCGGCGGTTAAGAATCGTTA Ick1.seq  
 88 AATTATTCATCGGAATTTGAATCGGCGGTTAAGAATCGTTA ICK1b.seq  
 70 TTAAGTAAATCCATGGAGAATTATTCATCGGAATTTGAATCGGCGGTTAAGAATCGTTA ICK1c.seq

361 GATTGTTGTTGTAGCGGGAGGAAAACGATGGAGGAGACGGTGACGGCGGAGGAGGAG Ick1.seq  
 130 GATTGTTGTTGTAGCGGGAGGAAAACGATGGAGGAGACGGTGACGGCGGAGGAGGAG ICK1b.seq  
 130 GATTGTTGTTGTAGCGGGAGGAAAACGATGGAGGAG GAGGAG ICK1c.seq

421 AAGGCGAAATTGATGACGGAGATGCCAACGGAATCGGAAATTGAAGATTTTTTGTGGAA Ick1.seq  
 190 AAGGCGAAATTGATGACGGAGATGCCAACGGAATCGGAAATTGAAGATTTTTTGTGGAA ICK1b.seq  
 172 AAGGCGAAATTGATGACGGAGATGCCAACGGAATCGGAAATTGAAGATTTTTTGTGGAA ICK1c.seq

461 GCTGAGAAACAACCTCAAAGAAAAATTCAAGAAGAAGTACAATTCGATTTCGAGAAGGAG Ick1.seq  
 250 GCTGAGAAACAACCTCAAAGAAAAATTCAAGAAGAAGTACAATTCGATTTCGAGAAGGAG ICK1b.seq  
 232 GCTGAGAAACAACCTCAAAGAAAAATTCAAGAAGAAGTACAATTCGATTTCGAGAAGGAG ICK1c.seq

541 AAGCCATTAGAAGGACGTTACGAATGGGTAAAGTTAGAGTGAAGAAGAAGAAGTTTA Ick1.seq  
 310 AAGCCATTAGAAGGACGTTACGAATGGGTAAAGTTAGAGTGAAGAAGAAGAAGTTTA ICK1b.seq  
 292 AAGCCATTAGAAGGACGTTACGAATGGGTAAAGTTAGAGTGAAGAAGAAGAAGTTTA ICK1c.seq

601 TGGTTTTTTTTTAACTTTTATAGATTTTAATATTTTCAGGGAATAAGTTAATTTTATTTG Ick1.seq  
 370 TGGTTTTTTTTTAACTTTTATAGATTTTAATATTTTCAGGGAATAAGTTAATTTTATTTG ICK1b.seq  
 352 TGGTTTTTTTTTAACTTTTATAGATTTT ICK1c.seq

661 TTGATTGGAATATAAGATTTGTAGGAGGAATGTTTTAGAAAGTACGAAATTGCACAGA Ick1.seq  
 430 TTGATTGGAATATA ICK1b.seq  
 379 ICK1c.seq

Alignment of *ICK1* cDNA sequence with *ICK1b* and *ICK1c* showing the differences

Figure 2

GTGGAATCTAGGATAATTCTGTCTCCGTGTGTACAGGCGACGAATCGCGGTGGAATTGTG  
GCGAGAAATTCAGCAGGAGCGTCGGAGACGAGTGTGTTATAGTACGACGGCGAGATTCT  
CCTCCGGTTGAAGAACAGTGTCAAATCGAAGAAGAAGATTCTCGGTTTCGTGTTGTTCT  
ACATCGGAAGAGAAATCGAAACGGAGAATCGAATTTGTAGATCTTGAGGAAAATAACGGT  
GACGATCGTGAAACAGAAACGTCGTGGATTTACGATGATTTGAATAAGAGTGAGGAATCG  
ATGAACATGGATTCTTCTTCGGTGGCTGTTGAAGATGTAGAGTCTCGCCGCAGGTTAAGG  
AAGAGTCTCCATGAGACGGTGAAGGAAGCTGAGTTAGAAGACTTTTTTCAGGTGGCGGAG  
AAAGATCTTCGGAATAAGTTGTTGGAATGTTCTATGAAGTATAACTTCGATTTTCGAGAAA  
GATGAGCCACTTGGTGGAGGAAGATACGAGTGGGTAAATTGAATCCATGAAGAAGACGA  
TGATGATAATGATGATCATTGTTTTACCAAAGTACTTATTATTTCTTCTGTAATAAT  
CTTTGCTTTGATTTTTCTTTTAACAAAATCCAAATGTAGATATCTTCTCTCGAATAATC  
AATAACATGTAATCAACTTTTGTGTTGTAATTCCTTGAGGTAATTAATTAGATTCGTGTT  
TTTCTCGATTAATAAACTATAAGTTTATAACTAAA

cDNA sequence of *ICK2*

Figure 3

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### cDNA sequence of *ICN2*

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### cDNA sequence of ICN6

Figure 5

ATTAAAGAGTCTGGTTCAGGTCTCGCGTTGACTCGGTTAACTCGGCTCCTGTAGCTCAG  
 AGCTCTAATGAAGATGAATGTTTTGACAATTCGTGAGTGTCCAAGTTTCTTGTGGTGAA  
 AACAGTCTCGGTTTTGAATCAAGACACAGCACAAGGGAGAGCACGCCTTGTAACCTTGT  
 GAGGATATGGAGATCATGGTTACACCAGGGTCTAGCACGAGGTCGATGTGCAGAGCAACC  
 AAAGAGTACACAAGGGAACAAGATAACGTGATCCCGACCACTAGTGAAATGGAGGAGTTC  
 TTTGCATATGCAGAGCAGCAGCAACAGAGGCTATTATGGAGAAGTACAACCTCGACATT  
 GTGAATGATATCCCCCTCAGCGGACGTTACGAATGGGTGCAAGTCAAACCATGAAGTTCA  
 AAAGGAAACAGCTCCAAAAGACATGGTGTGAAGTTAGAGAATTGTGATGGAGTTAACAG  
 AACTAACCAAACATCAGAAATCGTGTTAATCCTTAAGTTAATAATGTGGGTTA

cDNA sequence of *ICN7*

**SEQ ID NO. 15: The nucleotide sequence of *Chenopodium rubrum* CDKI1  
 (GenBank AJ002173)**

gcacgagcgaaattgcggtgtaggaggttaaaccagagctcgagactgccctagctatggcggcagctgctactcaac  
 ttcgtctccggcgaagaagatcaagaaggttcgaagtcgtctataatattcctcaactaagaagtcgtcgaagaatt  
 tgcggcgccggagaatttcgccgaattagaaacgacgccgttggaagttgcggcggttgtaggaggaagaggttgcg  
 aattgctcgagtagcgaagtaattactacagctaggtcgatttccgccgtctgttgcgaagcaattatgatcagtt  
 gaggctcagcgagccagaagtagttaaggatgatgatggttgggaaatcgtagcagatccagaggttgagagtggtg  
 aggcgtcgtcaaagcaaaaggagagccatagaacagaagcgagagaagctacaaaattagcagaccaggattatccggcg  
 acgaaatcaacggtacagatcaagatgccgtctgattcagaatcgaagaattcttgcgtgtgctgaaaaagatctcca  
 gaaacgcttcagcgaaaagtacaatttcgacatagttaaggacgtgccactgaaaggtcggttatgattgggtccaataa  
 atccatgaataaaaccactggtgatgtgatgatgaatgactgaattctccacaattacgcaaaattagccact  
 gaaattgcaaagtaaatcttaatttttagccttttcttcttttagcagaagttgatctattctcacaccgaaaaaaaa  
 aaaa

**SEQ ID NO. 16: The amino acid sequence of *Chenopodium rubrum* CDKI1**  
 MAAAATPTSS PAKKIKKVSK SSYNIPQLRS RRKNLSAPEN FAELETTPL  
 VAAVVEEEVANCSSSEVIT TARSDFPSC CSSNYDQLSS SEPEVVKDDD  
 GLGNRTADPE VESGEASSKQ KESHRTEARE ATKLDDQDYP ATKSTVQIKM  
 PSDSEIEEFF AVAEKDLQKR FSEKYNFDIV KDVPLKGRYD WVPINP

Figure 6

```

.....S.....V...S..SV..S.S.....C.....E....S.S Consensus
1 MVRKYRKA-----KGIVEAGVSYSTMQLRRIV-----YVRSEKSSSVVGDNGSSSCGSGSNEYKKKELIHLIEEDKDG D ICK1.pro
1 V-----ESRIILSPCQATNRGGIVARNAGA-----SETSVIVRRDPPV-----EQ-----QIIEEDSSV ICK2.pro
1 KKKQERAHKNPREKMSERKRELAEEASTSFSPKKTKLNDSSDSDSHDVI FAVSSVASAALASDE SVTIGESDQSS ICN2.pro
1 LS--PEKTIMSLREMSETPKPRDSEYECN-----IKRMLDDDDVLRSPTRLIS--SSSSSLAYVDSGGF SVALSEEDDHLS ICN6.pro
1 IKESGSRSRVD-----VNPVPAQSNEDEDFDNFV----- ICN7.pro

.....C..SE.K.....F..DLE.....E.....F.K.....E.L.E.....S.....R.....K.K.....PT.AE.E Consensus
74 TETSTYRGT-----RKLCENREEKEELSKSMENYSSE-----ESAVKSDCCSGRKTMEETV-TAEESALMTMEESHI ICK1.pro
58 ---CUSTE-----SKRRIE-----VNNNGDDRETETSWIYDDLN SEESM--NMDSSSVAVEDVESRR-----LRSLHETVKEHL ICK2.pro
90 ISSGFTSSEIAKNSSGV-----DHQIET TETSTFITSNRETSPVSGGTTTMESSATK-----KOPGVRKTAAAT ICK2.pro
83 ISSGSSSNEIATRLP-----S-----AHHEI-S TEISTILLTNNRQGLSSSNIGTA-EMDSATTEM DQRTKTKKMEKSFQALD ICN6.pro
34 VQVSGEN-----SLGF SRHSTRSTPCNFV-----DM-IMVTPGSTRSMCRATKEYTREQDNVITTSN ICN7.pro

DFF..AE.-.Q....F.E---KYNFDIVND.PLEG-RYEWV.L.P- Consensus
154 VEEK--LKEK--FEKE--KLE. ICK1.pro
134 OV K--DLRNKLLCSM--FEKE--KLE. ICK2.pro
174 LSEL SQDDKKQIT-----K-----DRL ICN2.pro
169 SAERYEKR-----QSK. ICN6.pro
99 EAY--QQRLLM-----QVK. ICN7.pro

```

Consensus 'Consensus #1': When 60% (3) match the residue of the Consensus show the residue of the Consensus, otherwise show '.'.

Decoration 'Decoration #1': Shade (with black at 40% fill) residues that match the consensus named 'Consensus #1' exactly.

Alignment of deduced amino acid sequences of ICK1, ICK2, ICN2, ICN6 and ICN7

Figure 7






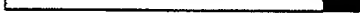




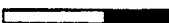





<u>Bait</u>	<u>ICK1 (Numbers indicate the amino acid positions)</u>	<u>Filter assay</u>	<u>Activity</u>
cdc2a	/		0.0
/	(3-191)		0.0
cdc2a	(3-191)		12.4
cdc2a	(73-191)		40.6
cdc2a	(109-191)		42.6
cdc2a	(154-191)		10.7
cdc2a	(3-175)		0.3
cdc2a	(3-162)		0.3
cdc2a	(3-152)		0.0
cyclin δ3	/		0.8
cyclin δ3	(3-191)		100.0
cyclin δ3	(73-191)		397.3
cyclin δ3	(109-191)		480.7
cyclin δ3	(154-191)		7.1
cyclin δ3	(3-175)		19.9
cyclin δ3	(3-162)		2.5
cyclin δ3	(3-152)		2.2
ATMPK2	(3-191)		0.0

Figure 8